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INTRODUCTION

The activities of soil microorganisms directly influence phosphorus (P) biogeochemistry and, therefore, P availability to crops, whilst soil P availability may reciprocally alter microbial communities, as shown by Mander et al. (2012) in a long term P fertilizer trial. Hinsinger et al. (2011) reviewed the potential roles of rhizosphere microorganisms on P facilitation in cereal/legume intercropping systems, which involve changes of microbial biomass, community structure and activity of specific functional communities, e.g. shifts of rhizosphere microbial community or functional groups linked to the N cycle (Song et al., 2007) and P cycle (Wang et al., 2007). The aim of this experiment conducted in a long term P fertilizer trial was: (i) to investigate the effect of intercropping on microbial communities in the rhizosphere and (ii) to test whether soil P availability influenced such effect.

METHODS

The experiment was conducted in the long term P fertilizer trial of INRA research centre at Auzeville (43.5°N, 1.43°E) in south western France. The three P regimes corresponded to fertilizer levels applied since 1968: P0 (no fertilization), P1 (fertilization rate to balance the mean annual P removal by crops) and P4 (fertilization rate representing three- to four-fold that of P1). Durum wheat and faba bean were grown alone or as durum wheat/faba bean intercrops in this field trial. Their rhizospheres were collected at the faba bean flowering stage, as well as the corresponding bulk soils. Soil DNA and RNA were extracted in these various samples and qPCR was used to assess the number of gene copies of fungi, bacteria, as well as several bacterial phyla (Actinobacteria, α-Proteobacteria and Firmicutes (strongly dominated with P-cycling taxa)) and beta propeller phytase (BPP).

RESULTS AND DISCUSSION

The results of ANOVA for the studied molecular indicators of microbial community across the tested factors are reported in Table 1: P levels (P0, P1 and P4), soil (rhizosphere *vs* bulk soil), species (durum wheat vs faba bean) and cropping systems (intercrop vs solo crop). The total molecular biomass (DNA), total bacteria (16S) and fungi (18S) significantly increased with P addition, with a significant difference between nil P fertiliser (P0) and P-fertilized plots (P1 and P4). The same trend was observed for the number of gene copies of Actinobacteria, α-Proteobacteria and BPP. This result was opposite to those of Mander et al. (2012) in pasture systems, who showed that the abundance of Actinobacteria increased under P limitation. The number of gene copies of Actinobacteria was also affected by the crop species and by intercropping. Intercropping had no significant effect on any other tested variable. The abundance of Firmicutes was significantly decreased upon P addition, but not significantly altered by any other tested factor. As expected, higher microbial biomass and

gene copies of bacterial phyla (except for Firmicutes) was observed in the rhizosphere, compared to bulk soil. Variation in all bacterial phyla was significantly linked to variation in soil total P (P = 0.002;RDA analysis).

Table 1. ANOVA results for the analyses of microbial community composition. The stars indicate significant difference between P levels (P0, P1 and P4), between different soil (rhizosphere vs bulk soil) samples, between different species (durum wheat vs faba bean) or between different cropping systems (intercrop vs sole crop) with *(P<0.05), **(P<0.001), *(P<0.0001). α-Proteo: α-Proteobacteria; Actino: Actinobacteria.**

Factors	P level	Soil	Species	System
DNA	***	***	n.s.	n.s.
RNA	n.s.	***	n.s.	n.s.
Bacteria	***	***	n.s.	n.s.
Fungi	***	***	n.s.	n.s.
Fungi/Bacteria	n.s.	***	n.s.	n.s.
α-Proteobacteria	***	***	n.s.	n.s.
Actinobacteria	***	***	*	*
Firmicutes	***	n.s.	n.s.	n.s.
BPP	*	n.s.	n.s.	n.s.
α-Proteo/Bacteria	n.s.	n.s.	n.s.	n.s.
Actino/Bacteria	n.s.	n.s.	*	n.s.
Firmicutes/Bacteria	n.s.	***	n.s.	n.s.

CONCLUSIONS

Our result showed that intercropping and plant species had little or no significant influence on the abundance of soil microorganisms, except for Actinobacteria, in spite of a frequently significant rhizosphere effect. In contrast, soil P availability significantly positively influenced the abundance of Actinobacteria, α-Proteobacteriaand BPP gene copies and negatively influenced Firmicutes copies. The increase of abundance of Actinobacteria, α-Proteobacteria and BPP gene with P addition coincided with facilitation as evidenced by overyielding of the intercrop that occurred significantly only for the P-fertilized plots in this field experiment. However, we have no evidence for a causal relationship between microbial community changes and crop performance in this intercropping system.

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